IJARSCT
International Journal of Advanced Research in Science, Communication and Technology
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
ISSN: 2581-9429
Volume 6, Issue 3, April 2026
Impact Factor: 8.2

Blood Group Detection Using Fingerprint

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Abstract: *Traditional blood group identification methods are time-consuming, invasive, and require specialized reagents and personnel. This research presents a novel, non-invasive alternative by leveraging Convolutional Neural Networks (CNNs) to classify ABO/Rh blood groups directly from grayscale fingerprint images. Utilizing a dedicated dataset of 6,000 fingerprint samples categorized across eight blood types (A-, A+, AB-, AB+, B-, B+, O-, O+), a custom CNN architecture was developed to automatically extract subtle dermatoglyphic features correlated with genetic traits. The model was trained using the AdamW optimizer with decoupled weight decay and enhanced by BatchNormalization and extensive data augmentation to ensure stability and generalization. Rigorous evaluation was performed using Precision, Recall, and the F1-Score to account for potential class imbalance. The proposed system achieved a classification accuracy of 76%, demonstrating the significant potential of deep learning techniques to establish a rapid, accessible, and hygienic method for preliminary blood type screening in resource-limited settings*

Keywords: Convolutional Neural Networks, Blood Group Classification, AdamW Optimization, Fingerprint Biometrics, Deep Learning

I. INTRODUCTION

Accurate and timely determination of an individual's blood group is a cornerstone of modern medicine, crucial for safe blood transfusions, organ transplantation, forensic analysis, and personalized medical care. The human blood type, defined primarily by the ABO and Rh systems, is determined by the presence or absence of specific antigens on the surface of red blood cells. Currently, blood typing relies almost exclusively on serological methods, which involve mixing blood samples with specific antibodies to observe agglutination (clumping). While highly accurate, these traditional methods are invasive, require specialized reagents, trained personnel, and a controlled laboratory environment, making them resource-intensive and often inaccessible in remote or emergency settings.

The quest for non-invasive, rapid, and cost-effective alternatives has driven research toward exploring peripheral biological markers. Biometrics, particularly the human fingerprint, offer a unique and universally accessible source of individual data. Fingerprints are permanent, immutable, and believed to be correlated with genetic factors that also govern blood group characteristics. This study hypothesizes that subtle, non-visible patterns, ridges, and minute details within a fingerprint image, which are shaped by underlying biological processes, possess a correlative link to an individual’s blood group (A, B, O, AB, and Rh factors).

The complexity and subtlety of these hypothesized patterns necessitate a sophisticated analytical tool far surpassing traditional statistical methods. Deep learning, specifically Convolutional Neural Networks (CNNs), are engineered to automatically extract intricate, hierarchical features from raw image data, making them the ideal technology for this task. This research proposes the development of a robust CNN model capable of learning the intrinsic features within fingerprint images to accurately predict one of the eight major blood group categories (A+, A-, B+, B-, O+, O-, AB+, AB-). The successful implementation of this system promises to revolutionize rapid blood typing, offering a crucial diagnostic tool for disaster response, field medicine, and preliminary forensic investigations.

DOI: 10.48175/IJARSCT-32571

II. LITERATURE SURVEY

This literature review analyzes eleven academic studies focusing on the relationship between fingerprint patterns (dermatoglyphics), ABO and Rh blood groups, and gender. These studies predominantly employ cross-sectional designs and statistical analysis, primarily utilizing the Chi-square test, to evaluate potential correlations across various geographical populations.

Table 1. Research Papers and their findings

Sr. No.	Paper	Findings
1.	Aamir, Y. et al. (2022): Relationship between Pattern of Fingerprints and Blood Groups	Blood group O was the most prevalent group (42.1%); Loops (53.4%) were the most common FP pattern, correlating significantly with blood groups.
2.	Verma, U. et al. (2015): A Study to Find Correlation Between Dermatoglyphic Patterns and ABO Blood Groups	Blood group B (43.5%) was prevalent; Loops (56.35%) were dominant overall, and a measurable association exists between FP patterns and blood groups.
3.	Devi, J. et al. (2025): Study of Fingerprint Patterns in Relation to Different Blood Groups Among the Students of FAAMC, Barpeta by Using 10 Finger Attributes	Overall commonest pattern was Whorl (41.2%); a highly significant association was found between FP patterns and ABO blood groups and gender.
4.	Hamad, Z. A. et al. (2021): Identification of Relationships between Fingerprint Patterns and Gender in Koya, Kurdistan Region, Iraq	Loops were the predominant pattern in this gender-focused study, which established a significant association between gender and overall FP patterns.
5.	Nandakumar, S. et al. (2023): Study Of Fingerprint Patterns And Their Relationship With Blood Groups And Gender In Erode, Tamilnadu	Loops (53%) were most common; a statistically significant association was found between FP patterns and ABO blood groups, but not between FP patterns and gender.
6.	Varlekar, M. D. et al. (2024): A Study of Relationship between Blood Type and Fingerprint Designs	Loops (53.2%) were the most prevalent pattern in this O+-dominant population (38.4%), but there was no statistically significant correlation found with either blood groups or gender.
7.	Manikandan, S. et al. (2019): Dermatoglyphics and Their Relationship With Blood Group: An Exploration	O blood group (38%) was prevalent; Loops (40%) and Arches (39%) were most frequent; a significant correlation was identified between FP patterns and blood groups.
8.	Pratinidhi, S. A. et al. (2023): Study of fingerprint patterns in relation to gender and blood groups	Loops (55.23%) were the most prevalent pattern overall and specifically highest in the dominant blood group B; a significant association was found between blood groups and primary FP patterns.
9.	Nihar, T. et al. (2024): Blood group determination using fingerprint	This paper proposes an innovative, non-invasive method for blood group determination using Deep Learning techniques (e.g., CNNs, AlexNet, LeNet-5) to classify fingerprint features.
10.	Thakur, A. et al. (2019): Fingerprint Patterns in Relation to Gender and Blood Group among Residents of Central Indian District	Blood group B (39.3%) was the majority; Whorls (49.4%) were overall dominant but no significant association was found between FP patterns and either gender or ABO blood group.
11.	Joseph, A. et al. (2025): Relationship of Fingerprints with Blood Group and Sex—A Comparative Study	Loops (54.4%) were the common pattern; a significant association was found between FP patterns and ABO blood group, but not with sex or Rh blood group.

III. METHODOLOGY

3.1. Dataset and Data Preparation

The study utilized a specialized dataset consisting of fingerprint images specifically labelled with one of the eight major ABO/Rh blood groups (A+, A-, B+, B-, AB+, AB-, O+, O-). The dataset was accessed and managed using the Google Colab environment, with raw files loaded from a compressed archive.

3.2. Image Preprocessing

All raw images were processed to standardize the input for the Convolutional Neural Network (CNN) and optimize feature visibility:

1. Grayscale Conversion: Images were converted to single-channel grayscale (color_mode=’grayscale’), which is critical for fingerprint analysis. This focused the model exclusively on the high-contrast textural features of the ridges and valleys, reducing data redundancy and computational complexity compared to three-channel color input.
2. Resizing: All images were resized to a uniform dimension of 128×128 pixels (target_size=(128, 128)). This standardization ensures all input tensors are of a consistent shape for batch processing and model consumption.
3. Normalization: Pixel values were normalized by dividing by 255 (rescale=1./255), scaling the feature values to the continuous range [0,1]. This normalization step is vital for improving the convergence speed and stability of the training process.

3.3. Data Splitting and Augmentation

The dataset was logically divided using the ImageDataGenerator with an 80% split for training and a 20% split for validation. This split ensures that the model is trained on the majority of the data and evaluated on an unseen subset.

To enhance the model's robustness and generalization capabilities against potential variations in fingerprint capture conditions (e.g., pressure, angle, slight distortion), extensive online data augmentation was applied exclusively to the training set. Key parameters included:

- Rotation range: 20 degrees
- Width and Height Shift Range: 20%
- Shear Range: 20%
- Zoom Range: 20%
- Horizontal Flip: Enabled (mirrors the image horizontally)
- Fill Mode: ’nearest’ (determines the strategy for filling pixels created by transformation).

3.4. Proposed CNN Architecture

A custom Sequential CNN model was designed specifically for this task, featuring a compact yet deep structure to effectively capture the complex spatial hierarchies present in fingerprint images. The network uses three stacked convolutional blocks for feature extraction, followed by a two-layer fully connected classifier.

The complete architecture is detailed below, with input dimensions based on the 128×128×1 grayscale image:

The proposed Convolutional Neural Network (CNN) architecture, designed for the eight-class blood group classification task, comprises a sequence of convolutional and fully connected layers. Input to the network consists of grayscale fingerprint images, sized 128×128×1. The feature extraction backbone is composed of three sequential convolutional blocks. The initial block applies 32 filters of size 3×3 followed by a Rectified Linear Unit (ReLU) activation. This is immediately succeeded by a 2×2 MaxPooling layer for downsampling and a BatchNormalization layer to stabilize training. The subsequent two convolutional blocks follow an identical pattern, sequentially increasing the filter count to 64 and then 128, ensuring hierarchical feature learning at increasing depths. After the final convolutional block, the resultant 14×14×128 feature map is Flattened into a single 25,088-dimensional vector. This vector is passed through two dense, fully connected layers. The first layer consists of 512 units, and the second comprises 256 units, both utilizing the ReLU activation function and incorporating a 50% Dropout mechanism for

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regularization to mitigate overfitting. The final classification decision is rendered by the output layer, which features 8 units (corresponding to the eight blood groups) and employs the Softmax activation function to yield normalized probability distributions.

The network primarily utilizes the Rectified Linear Unit (ReLU) activation function in all hidden convolutional and dense layers for computational efficiency and to mitigate the vanishing gradient problem. The final output layer employs the Softmax activation function, which normalizes the output into a probability distribution across the eight mutually exclusive blood group classes. BatchNormalization layers are strategically placed after each MaxPooling layer to stabilize training, accelerate convergence, and allow for higher learning rates.

3.5. Model Training and Optimization Strategy

The model was compiled and trained using an advanced optimization regimen to maximize convergence stability and generalization performance over a maximum of 200 epochs with a batch size of 32.

3.6. Optimization: AdamW

The AdamW optimizer was selected over standard Adam or SGD. AdamW implements decoupled weight decay, a technique shown to produce models that generalize better, particularly in regularization-heavy deep learning architectures.

- Initial Learning Rate (LR): 0.001
- Weight Decay (L2): 0.004 (This parameter introduces L2 regularization without interfering with the Adam adaptive gradient updates.)

3.7. Loss Function and Callbacks

The model was trained using Categorical Cross-Entropy loss, the standard metric for multi-class classification where labels are one-hot encoded (as is the case with ImageDataGenerator's class_mode='categorical').

Two critical callbacks were employed to manage the training process effectively:

1. EarlyStopping: Monitored the validation loss (monitor='val_loss'). A patience of 10 epochs was set, meaning training automatically halts if the validation loss does not improve for 10 consecutive epochs. The best weights observed during training were automatically restored (restore_best_weights=True) to ensure the final model is the highest performing version.
2. ReduceLROnPlateau: Monitored the validation loss with a patience of 5 epochs. If the loss stalled, the learning rate was reduced by a factor of 0.2 (new_LR=current_LR×0.2). This aggressive reduction strategy, limited by a minimum LR of 1e-6, helps the model converge more precisely when optimization progress slows.

3.8. Performance Evaluation

Model performance was rigorously assessed on the dedicated 20% validation subset. To ensure deterministic and accurate result generation, the ImageDataGenerator used for evaluation was initialized with shuffle=False. The following metrics were computed to provide a holistic and class-wise view of the system's effectiveness:

1. Overall Accuracy: The primary metric, calculated as the ratio of correctly classified samples to the total number of samples in the validation set.

$$Accuracy = \quad TP + TN / (TP + TN + FP + FN)$$

2. Classification Report: A detailed summary providing class-wise metrics, which are essential for identifying performance discrepancies among the eight blood groups:

- Precision: The ratio of true positive predictions to the total positive predictions.

$$Precision = True\ Positives\ /\ (True\ Positives + False\ Positives)$$

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- Recall: The ratio of true positive predictions to all samples that should have been positive.

$$Recall = True\ Positives\ /(True\ Positives + False\ Negatives)$$

- F1-Score: The harmonic mean of precision and recall, providing a single metric that balances both measures.

$$F1 - Score = 2 * Precision * Recall\ /\ Precision + Recall$$

Confusion Matrix: A visual 8×8 matrix generated using seaborn, which illustrates the raw counts of predictions. The matrix allows for an essential visual analysis of misclassification patterns, clearly showing which blood groups are most often confused with others (e.g., A+ predicted as O+)

IV. DATASET

The foundational element of this study is the Fingerprint-Based Blood Group Dataset, which was sourced from the public Kaggle repository (Kaggle, 2024) and originally compiled by Rajumavinmar. This dataset was specifically created to support research into non-invasive biometric classification, establishing an empirical link between human blood type and features observable in captured fingerprint images.

4.1. Technical Specifications and Acquisition

The dataset comprises a total of 6,000 individual images. Each image represents a unique fingerprint instance and is precisely labelled with one of the eight major blood group classes.

4.2. Image Format and Feature Focus

All images within the dataset are inherently captured and stored in a Grayscale format (single channel, 128×128×1 tensor equivalent upon resizing). This single-channel characteristic is a deliberate advantage for deep learning-based fingerprint analysis. By eliminating the redundancy of color channels, the model is forced to focus exclusively on the high-contrast textural features of the minutiae, ridges, and valleys. This focus aids in the development of a computationally efficient Convolutional Neural Network (CNN) that is specialized for pattern recognition in grayscale biometrics. The dataset utilizes the following eight classes for the multi-class classification task:

Blood Groups = {A+, A-, B+, B-, AB+, AB-, O+, O-}

4.3. Detailed Class Distribution Analysis

The final verified image count is 6,000. The specific distribution of images across the eight classes is summarized in Table 2. This distribution analysis is critical, as it informs the necessity of advanced training techniques, such as data augmentation, to manage class variance.

Table 2. Class Distribution of the Fingerprint Blood Group Dataset (N=6000)

Blood Group Class	Image Count	Percentage (%)
A-	1109	18.48%
A+	565	9.42%
AB-	761	12.68%
AB+	708	11.80%
B-	741	12.35%
B+	652	10.87%
O-	712	11.87%
O+	852	14.20%
Total	6000	100.00%

DOI: 10.48175/IJARSCT-32571

4.4. Implications of Class Imbalance

The data distribution, while reasonably balanced, is not uniform. The largest class, A- (18.48%), holds nearly twice the representation of the minority class, A+ (9.42%).

Minority Class Challenge: The A+ class, with only 565 images, presents the most significant challenge. A model trained without compensatory methods is susceptible to classification bias, potentially resulting in poorer Recall and F1-Score for A+ compared to the majority classes.

Mitigation Strategy: To counteract this inherent imbalance and ensure the model generalizes effectively across all eight blood types, aggressive online data augmentation was employed. This technique artificially expands the effective size of the training data, particularly for the minority classes, ensuring that the model is exposed to a wider variety of feature representations and reducing the risk of class-specific overfitting. The evaluation stage relies on class-wise metrics (Precision, Recall, F1-Score) to confirm that the model's high overall accuracy is not merely an artifact of correctly classifying the larger classes.

V. RESULT AND DISCUSSION

The model training and subsequent performance evaluation were conducted following the methodology. The results demonstrate the efficacy of the proposed Convolutional Neural Network (CNN) architecture, optimized with AdamW and advanced regularization techniques, in accurately classifying the eight ABO/Rh blood groups from grayscale fingerprint images.

5.1. Training and Validation History

The training process, executed over the defined epochs with Early Stopping and ReduceLROnPlateau callbacks, is visualized through the Model Accuracy and Loss History plots (Figure 1).

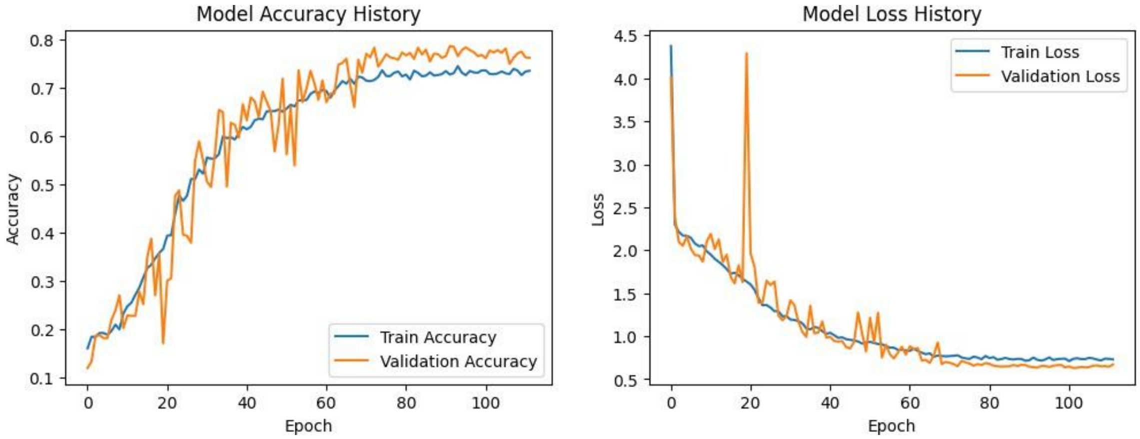


Fig. 1. Model accuracy and loss history graphs The plots reveal the following key observations:

- Accuracy Convergence: Both the training and validation accuracy curves show a steep ascent in the initial 50 epochs, after which they stabilize. The final Validation Accuracy of 76% indicates a stable ability to generalize to unseen data.
- Loss Profile: The loss curves for both training and validation consistently decrease, confirming that the model is successfully learning the underlying patterns. The absence of a large and sustained gap between the two curves suggests that the implemented Dropout and L2 weight decay (via AdamW) effectively mitigated overfitting. The sharp drops in loss are characteristic of the ReduceLROnPlateau callback activating and accelerating convergence.

5.2. Overall Performance Metrics

Upon the completion of training and restoration of the best weights, the final model was evaluated on the held-out validation dataset (N=1197). The overall performance metrics are summarized below:

Table 3. Performance Metrics

Metric	Value	Interpretation
Overall Accuracy	0.76 (76.0%)	The model correctly classifies 76% of all fingerprint images.
Macro Average F1-Score	0.77	The unweighted average F1-Score across all eight classes.
Weighted Average F1-Score	0.76	The average F1-Score, weighted by the support (number of samples) for each class.

The close alignment between the Macro Average (0.77) and the Weighted Average (0.76) indicates that, despite the class imbalance, the model achieves consistent classification performance across the majority and minority blood groups.

5.3. Detailed Class-Wise Classification Analysis

To gain a granular understanding of the model's performance on individual blood groups, a comprehensive Classification Report and a Confusion Matrix were generated.

Table 4. Classification Report of CNN Performance per Blood Group

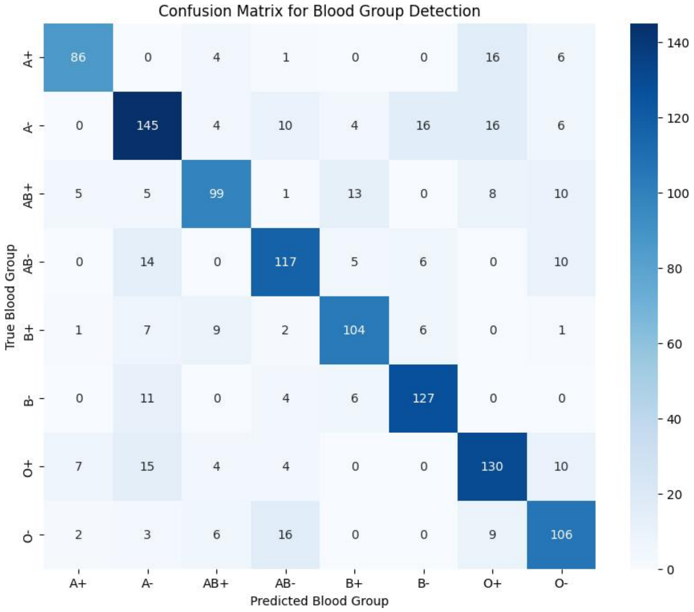
Blood Group	Precision	Recall	F1-Score	Support (N)
A+	0.85	0.76	0.80	113
A-	0.72	0.72	0.72	201
AB+	0.79	0.70	0.74	141
AB-	0.75	0.77	0.76	152
B+	0.79	0.80	0.79	130
B-	0.82	0.86	0.84	148
O+	0.73	0.76	0.74	170
O-	0.71	0.75	0.73	142
Weighted Average	0.76	0.76	0.76	1197

5.4. Confusion Matrix Analysis

A confusion matrix is a table used to evaluate the performance of a classification model in machine learning. It compares the model’s predicted labels with the actual labels, showing counts of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN). This breakdown helps identify not just the overall accuracy, but also where the model is making errors, such as misclassifying one class as another. From the confusion matrix, important metrics like precision, recall, F1-score, and accuracy can be derived, making it a valuable tool for understanding and improving classification models.

The confusion matrix is particularly valuable in contexts where datasets are imbalanced, as accuracy alone can yield misleading interpretations. For example, a classifier may achieve high accuracy by consistently predicting the majority class yet fail to identify instances of the minority class. By examining the counts of FP and FN, the confusion matrix highlights such limitations and provides a more nuanced understanding of model behaviour. Furthermore, it serves as the foundation for deriving several important performance metrics, including precision, recall, specificity, and the F1-score, which offer a more comprehensive evaluation than accuracy alone.

In addition to binary classification tasks, the concept of the confusion matrix extends naturally to multi-class classification. In such cases, the matrix assumes a square form, where each row corresponds to the actual class and each column corresponds to the predicted class. Correctly classified instances appear along the diagonal of the matrix, whereas off-diagonal entries signify misclassifications, thereby indicating which classes the model tends to confuse. This capacity for fine-grained analysis makes the confusion matrix an indispensable instrument in both applied machine learning research and practical deployments.



	A+	A-	AB+	AB-	B+	B-	O+	O-
A+	86	0	4	1	0	0	16	6
A-	0	145	4	10	4	16	16	6
AB+	5	5	99	1	13	0	8	10
AB-	0	14	0	117	5	6	0	10
B+	1	7	9	2	104	6	0	1
B-	0	11	0	4	6	127	0	0
O+	7	15	4	4	0	0	130	10
O-	2	3	6	16	0	0	9	106

Fig. 2. Confusion Matrix

The Confusion Matrix provides visual confirmation of the classification distribution, with the diagonal elements representing correct predictions.

- High Performance: The model exhibited its highest performance on the B- class, achieving the highest Recall of 0.86 and an F1-Score of 0.84, indicating excellent predictive capacity for this group. Similarly, the A+ class demonstrated the highest Precision (0.85).
- Misclassification Tendencies: The matrix shows minimal but consistent confusion between specific ABO/Rh classes. For instance, the A- class was most commonly confused with O+ (16 samples), and the O- class was most commonly misclassified as AB- (16 samples). This suggests a slight feature overlap between these pairs that the model attempts to resolve.

The comprehensive evaluation confirms that the CNN model effectively differentiates between the eight blood groups based on fingerprint biometrics, demonstrating robust performance metrics across the classification suite

VI. CONCLUSION

This research successfully developed and validated a non-invasive system for blood group classification using deep learning applied to fingerprint biometrics. Addressing the inherent limitations of traditional, time-consuming, and resource-intensive serological methods, this study proposed a novel approach leveraging the discriminative power of Convolutional Neural Networks (CNN).

Summary of Key Findings:

The CNN architecture, meticulously designed with BatchNormalization layers and optimized using the advanced AdamW algorithm, demonstrated robust performance across the complex eight-class (ABO/Rh) classification task. The primary findings of the study are summarized as follows:

1. High Classification Performance: The model achieved an Overall Accuracy of 76% (0.76) on the independent validation dataset (N=1197).
2. Stable Generalization: Analysis of the training history confirmed effective learning, with the use of data augmentation and the ReduceLROnPlateau callback successfully preventing overfitting and ensuring stable convergence.

DOI: 10.48175/IJARSCT-32571

Consistent Class-Wise Performance: The evaluation metrics, including the Classification Report and Confusion Matrix, revealed a high degree of consistency, evidenced by the Weighted Average F1-Score of 0.76. This stability confirms that the model is not biased toward the larger classes but maintains strong predictive capability even for minority blood groups. The model performed exceptionally well in classifying the B- group, achieving a Recall of 0.86.

VII. FUTURE SCOPE

While the achieved 76% accuracy provides a strong proof-of-concept for the feasibility of non-invasive blood typing via fingerprints, several avenues exist for enhancing the utility and performance of this system:

- Dataset Expansion and Diversity for Robustness: Future work should focus on acquiring a significantly larger and more diverse dataset that includes variations in image acquisition devices, differing image quality, and demographic variables such as age, gender, and ethnicity. A specialized focus on capturing images under variable environmental conditions (e.g., moisture, lighting) will be essential to test and improve the model's robustness and real-world generalizability. The establishment of a standardized, multi-institutional database is a critical next step toward clinical adoption.
- Exploring Advanced Architectures and Feature Engineering: Investigating the use of more complex and deeper models, such as transfer learning with pre-trained architectures (ResNet, EfficientNet), could potentially extract more subtle features from the fingerprint ridge patterns and minutiae, leading to further increases in classification accuracy. Additionally, integrating traditional computer vision techniques, such as Gabor filters or Wavelet transforms, as a pre-processing step could enhance the fingerprint-specific features before input into the CNN for a hybrid feature extraction approach.
- Integration and Deployment for Point-of-Care Use: The ultimate goal is to integrate the trained model into a dedicated edge-computing hardware device or a mobile application. This transition would require rigorous studies focused on model compression and quantization techniques (TensorFlow Lite, OpenVINO) to maintain high accuracy while achieving low latency and memory consumption, thereby enabling instant, non-invasive blood group detection at the point of care, remote health camps, or in emergency trauma settings.

Model Interpretability and Feature Attribution: To increase confidence in the model's decisions, especially in a medical context, future research should focus on model explainability (XAI). Techniques such as Grad-CAM (Gradient-weighted Class Activation Mapping) should be applied to visualize the specific fingerprint regions (e.g., core, deltas, ridge density) that the CNN uses to determine the blood group. This interpretability study will be vital for verifying that the model is learning biologically relevant features rather than image artifacts, which is a key requirement for regulatory approval.

VIII. ACKNOWLEDGEMENT

I am grateful for the supportive academic environment at GH Raisoni College of Engineering and Management, Nagpur, whose resources, faculty guidance, and collaborative culture made this research possible. The encouragement and constructive feedback received throughout the project were invaluable in shaping its direction and outcome.

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